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# 6

Atty Dkt 9000-0055  
PATENT

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9/6/02  
Date

[Signature]  
Signature

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Application of:

BOLTON et al.

Confirmation No.: 1484

Serial No.: 09/878,781

Group Art Unit: Unassigned

Filing Date: June 11, 2001

Examiner: Unassigned

Title: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN  
AGAINST STREPTOCOCCUS INFECTION

**SUBMISSION OF CORRECTED DRAWINGS**

Assistant Commissioner for Patents  
Box Issue Fee  
Washington, D.C. 20231

Attention: Official Draftsman

Sir:

Enclosed are 34 sheets of corrected drawings, in compliance with 37 CFR 1.84.

Respectfully submitted,

Date: 9/6/02

By: [Signature]  
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atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc gga cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
50 55 60	
ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca	240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro	
65 70 75 80	
gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala	
100 105 110	
aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act	528
Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr	
165 170 175	
aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	

FIG. 1A



cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tot gtt	768
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val	
245 250 255	
gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt	816
Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly	
260 265 270	
tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr	
275 280 285	
ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly	
290 295 300	
tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac	960
Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gct caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

FIG. 1B



atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc ggt cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
50 55 60	
ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca	240
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro	
65 70 75 80	
gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca	288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gca tca aaa gaa aaa gct gga caa cac atc cat gaa	336
Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu	
100 105 110	
aat ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt ttc aac act aac cac gat atc ctt gat gga act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt ctt gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct tta caa gac aac ttt ggt gtt aaa caa ggt ttg atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cac gca tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gca ggt gct gca aac atc gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	

FIG. 2A



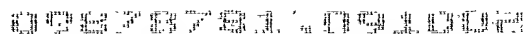
cct aac tca act ggt gct gca aaa gct atc gga ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
ttg aac ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gaa ttg gtt gca act ctt gaa aaa gac gta act gtc	768
Gly Ser Val Thr Glu Leu Val Ala Thr Leu Glu Lys Asp Val Thr Val	
245 250 255	
gaa gaa gta aat gca gct atg aaa gca gca gct aac gat tca tac ggt	816
Glu Glu Val Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tat act gaa gat cca atc gta tca tct gat atc gtt ggt att tca tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr	
275 280 285	
ggt tca ttg ttt gat gct act caa act aaa gtt caa act gtt gac ggt	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aac caa ttg gtt aaa gtt gtt tca tgg tac gat aac gaa atg tca tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act tca caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ser Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

FIG. 2B



atg gta gtt aaa gtt ggt att aac ggt ttc ggt cgt atc gga cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgt att caa aac gtt gaa ggt gtt gaa gta act cgt att	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gat ctt act gac cca aat atg ctt gca cac ttg ttg aaa tat gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttc gac ggt aca gtt gaa gtt aaa gat ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly	
50 55 60	
ttc gaa gtt aac gga aac ttc atc aaa gtt tct gct gaa aaa gat cca	240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro	
65 70 75 80	
gaa aac att gac tgg gca act gac ggt gta gaa atc gtt ctt gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala	
100 105 110	
aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga gat gat gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val	
115 120 125	
aaa act gtt gta ttt aac aca aac cat gac att ctt gac ggt aca gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
act gta att tca ggt gct tca tgt act act aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ttg caa gat aac ttt ggt gtt aaa caa ggt ttg atg aca	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cac gct tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gca agc aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val	
195 200 205	

FIG. 3A



**FIG. 3B**



atg gta gtt aaa gtt ggt att aac ggt ttt ggc cgt atc gga cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gct ttc cgt cgt att caa aat gta gaa ggt gtt gaa gtt act cgc atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aat atg ctt gca cac ttg tta aaa tac gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttt gac ggt act gta gaa gtt aaa gat ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly	
50 55 60	
ttt gac gtt aac gga aaa ttc att aaa gtt tct gct gaa aaa gat cca	240
Phe Asp Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Lys Asp Pro	
65 70 75 80	
gaa caa att gac tgg gca act gac ggt gtt gaa atc gtt ctt gaa gca	288
Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gaa	336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Glu Lys His Leu His Glu	
100 105 110	
aat ggt gct aaa aaa gtt gtt atc act gct cct ggt gga gat gac gtg	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val	
115 120 125	
aaa aca gtt gta ttt aac act aac cat gat atc ctt gat gga act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt att tca ggt gct tca tgt act aca aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct tta caa gat aac ttt ggc gta aaa caa ggt tta atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
aca atc cac gct tac act ggt gat caa atg ctt ctt gat gga cct cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac tta cgt cgt gcc cgt gct ggt gct aac aat att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val	
195 200 205	

FIG. 4A







00007027921 100010002

atg gta gtt aaa gtt ggt att aac ggt ttc gga cgt atc ggt cgt ctt	48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu	
1 5 10 15	
gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttt gac ggt aca gtt gaa gtt aaa gat ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly	
50 55 60	
ttc gaa gtt aac gga agc ttt gtt aaa gtt tct gca gaa cgc gaa cca	240
Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro	
65 70 75 80	
gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca	288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala	
85 90 95	
aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct	336
Thr Gly Phe Phe Ala Ser Lys Ala Ala Glu Gln His Ile His Ala	
100 105 110	
aac ggt gcg aaa aaa gtt gtt atc aca gct cct ggt gga aat gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt tac aac act aac cat gat att ctt gat gga act gaa	432
Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gca tta caa gat aac ttt ggt gta aaa caa ggt tta atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cat ggt tac act ggt gac caa atg gtt ctt gac gga cca cac	576
Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gat ctt cgt cgt gct cgt gca gct gca gca aac atc gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val	
195 200 205	

FIG. 5A



cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cca gaa Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu 210 215 220	672
tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr 225 230 235 240	720
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gat act tca gta Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val 245 250 255	768
gaa gaa atc aat gca gct atg aaa gca gca gct aac gat tca tac ggt Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Asn Asp Ser Tyr Gly 260 265 270	816
tac act gaa gat gct atc gta tca tca gat atc gta ggt att tct tac Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr 275 280 285	864
ggt tca tta ttt gat gct act caa act aaa gta caa act gtt gat gga Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly 290 295 300	912
aat caa ttg gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr 305 310 315 320	960
act gct caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys 325 330 335	1008
taa	1011

FIG. 5B

FIG. 6A



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	151				200
DysGapC	ACTCAAGGAC	GTTTTGACGG	AACTGTTGAA	GTTAAAGAAG	GTGGATTGGA
SpyGapC	-----	-----t--	a--a-----	-----	-----t--
SeqGapC	-----a-	-----	a--t-----	-----	-----t--
ParaUbGapC	-----	-----	--t--a---	-----t-	-----t--
UberGapC	-----	-----c---	--a-----	-----t-	-----c--
AgalGapCDNA	-----	-----c---	--t-----	-----	-----c--
SiniGapC	-----	-----	--a-----	-----t-	-----c--
BovGapC	--c--c--ca	ag--ca---	c--a--ca-g	-cag-ga-c-	-gaagc-c-t
	201				250
DysGapC	AGTAAACGGA	AACTTCATCA	AAGTTTCTGC	TGAACGTGAT	CCAGAAAACA
SpyGapC	---a-----	-----	-----	-----t--	-----
SeqGapC	---a-----	-----	-----	-----t--	-----
ParaUbGapC	c-----	--a-----t-	-----	---aaa---	-----c-a-
UberGapC	-----	-----	-----	---aaa---	-----
AgalGapCDNA	-----t	c-a--tg-t-	-----	-----c--a	---c-----
SiniGapC	-----	-g--tg-t-	-----	a---c--a	---c-----
BovGapC	ca-c--t---	--ggc-----	cca-c-tcca	g--g--a---	--t-cc----
	251				300
DysGapC	TCGACTGGGC	AACTGACGGT	GTTGAAATCG	TTCTGGAAGC	AACTGGTTTC
SpyGapC	-c-----	-----t--g	-----	-----	-----
SeqGapC	-c-----	-----c---	-----	-----	-----
ParaUbGapC	-t-----	-----c---	-----	-----	-----
UberGapC	-t-----	-----c---	--a-----	-----	-----
AgalGapCDNA	-t-----	t-----t--c	--a-----	-----	-----
SiniGapC	-t-----	t-----t--	--a--c---	-----	---a-----
BovGapC	-ca-g---g	tga--ct---	-c---gtat-	-ag-g--gt-	c-----gg--
	301				350
DysGapC	TTTGCTAAAA	AAGAAGCTGC	TGAAAAACAC	TTACATGCTA	ACGGTGCTAA
SpyGapC	-----	-----a-	-----	-----	-----
SeqGapC	-----	-----	-----c-	-----	-----
ParaUbGapC	-----	---c-----	-----t	-----aa-	-t-----
UberGapC	-----	---c-----	-----t	-----	-----
AgalGapCDNA	-----atc-	---aaa-	--g-c----	a-c---aa-	-t-----
SiniGapC	--c---tct-	---c-----	---c-----	a-t--c---	-----g--
BovGapC	--ca---cc-	tg--gaag-	--gggct---	--ga-g-g-	...c--c--
	351				400
DysGapC	AAAAGTTGTT	ATCACAGCTC	CTGGTGGAAA	CGACGTTAAA	ACAGTTGTTT
SpyGapC	-----	-----	-----	---t-----	-----
SeqGapC	-----	-----	-----	-----	-----
ParaUbGapC	-----	---t-----	-----g-	t-----g--	-----a-
UberGapC	-----	-----	-----g-	t--t-----	--t-----a-
AgalGapCDNA	-----	-----	-----	-----	-----
SiniGapC	-----	-----	-----	t-----	-----
BovGapC	g-gg--ca-c	---t-t--a-	--tc-----c	---t-cccc	-tgt---ga

FIG. 6B



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	401				450
DysGapC	TCAACACTAA	CCACGA.CAT	TCTTGACGGT	ACTGAAACAG	TTATCTCAGG
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
ParaUbGapC	-t-----	---t---t-	c-----t-a	-----	---t-----
UberGapc	-t-----a--	---t---.	-----	--a---t-	-a-t-----
AgalGapCDNA	-----	---t---t-	c-----t-a	-----	-----
SiniGapC	a-----	---t---t-	-----t-a	-----	-----
BovGapC	-ggg-gtg--	-----a-g	..a-a-aac	--cctc-aga	--g--agcaa
	451				500
DysGapC	TGCTTCATGT	ACTACAAACT	GTTTAGCTCC	TATGGCTAAA	GCTCTTCACG
SpyGapC	-----	-----	-----	t-----	---c-t--c-
SeqGapC	-----	-----	-----	t-----	---c-t--c-
ParaUbGapC	-----	-----	-----	-----	---a-----
UberGapc	-----	-----t-	-----	-----	---g-----
AgalGapCDNA	-----	-----	---c-t---	-----	---a-----
SiniGapC	-----	-----	-----	-----	---a-a-----
BovGapC	---c--c--c	--c--c---	-c-g--c--	cc---c--g	-tca-c--t-
	501				550
DysGapC	ATGCATTGG	TATCCAAAA	GGTCTTATGA	CTACAATCCA	CGCTTATACT
SpyGapC	--gca--c--	-a--c--a--	---c-----	---a-----	-----
SeqGapC	--gca-----	-a--c--a--	---c-----	---a-----	-----
ParaUbGapC	-----	cg-a-----	---t-a-----	---a-----	-----
UberGapc	-----	-g-----	---t-g-----	-a--t-----	-----
AgalGapCDNA	-c-----	-g-----	---t-g-----	---t-----	---a-----
SiniGapC	-----	-g-a-----	---t-a-----	---t-----	t-g-----
BovGapC	-cc-----	ca-cgtgg-g	--ac-----	-c--tg-----	---cat-----
	551				600
DysGapC	GGTGACCAA	TGATCCTTGA	CGGACCACAC	CGTGGTGGTG	ACCTTCGTCTG
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	---g-----	t---ac-gt	g-----	-t-----
ParaUbGapC	---t-----	--c-t-----	t---t-----	-----	---t-a-----
UberGapc	-----	-----	-----	-----	-----
AgalGapCDNA	-----	-----	-----	-----	-----
SiniGapC	-----	--g-t-----	-----	-----	-t-----
BovGapC	-ccac---g-	a--ctg-g--	t--c--ctc-	...--gaagc	tgtgg--ga
	601				650
DysGapC	TGCTCGTGCT	GGTGCTGCAA	ACATTGTTCC	TAACTCAACT	GGTGCTGCTA
SpyGapC	---a--c--	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----cg--
ParaUbGapC	---c-----	-----aac-	-t--t-----	-----	-----
UberGapc	-----	-----aagc-	---t-----	-----	-----
AgalGapCDNA	-----a	-----	-----	-----	-----a-
SiniGapC	-----a	-c--a-----	-----	-----	-----
BovGapC	c-gc--a-gg	-c---ccag-	-t---a-c--	-gct--t---	--c-----c-

FIG. 6C



	651				700
DysGapC	AAGCTATCGG	TCTTGTTATC	CCAGAATTGA	ATGGTAAACT	TGATGGTGCCT
SpyGapC	-----	-----	-----c-t-	-c-----	-----
SeqGapC	-----	-----	-----g-	-c-----	-----
ParaUbGapC	---a-----	-----	--t-----	-t-----	-----
UberGapC	---a-----	-----a--	-----a-	-t-----	-----
AgalGapCDNA	-----	a-----	-----g-	-c-----	---t-----
SiniGapC	---a-----	-----	-----a-	-t-----	-----
BovGapC	-g--cg-g--	caag--c--	--t--gc-c-	-c--g--g--	cact--catg
	701				750
DysGapC	GCACAACGTG	TTCCTGTTCC	AACTGGATCA	GTAAC TGAGT	TGGTTGTAAC
SpyGapC	-----	-----	-----	-----g-	-----t---
SeqGapC	-----	-----	-----	-----g-	-----t---
ParaUbGapC	-----	-a-a-----	---a-t---	-----a---	-a-a--gt
UberGapC	-----	-----	-----	-----	-a-a--gt
AgalGapCDNA	-----	-----	-----	-----	-----
SiniGapC	-----	-----	-----	-----	-a-a--gt
BovGapC	--cttc--c-	-c--cac--	c-ac-tg--t	--tgtg--tc	--acctgccg
	751				800
DysGapC	TCTTGATAAA	AACGTTTCTG	TTGACGAAAT	CAACGCTGCT	ATGAAAGCTG
SpyGapC	-----c--	a--t-----	-----c--	-----t-t--	-----
SeqGapC	-----c--	a--t-----	-----c--	-----t--	-----
ParaUbGapC	---a-t---	--aac--a-	-a-----	t--t--ta	-----
UberGapC	-----	--aac--a-	-----	-----a	-----a-
AgalGapCDNA	-----	---taa---	-c-----g-	a--t-----	-----a-
SiniGapC	-----	--tac--a-	-a-----	---t-----	-----a-
BovGapC	c--g--g--	cct-ccaagt	a--t--g--	---gaag-tg	g---gcag-
	801				850
DysGapC	CTTCAAACGA	CAGTTTCGGT	TACACTGAAG	ATCCAATTGT	TTCTTCAGAT
SpyGapC	--t-----	-agc-t---	-----	-----	t-----
SeqGapC	--t-----	-agc-t---	-----	-----	t-----
ParaUbGapC	-ag-t--t--	-----at---	-----	-----	---a--t---
UberGapC	-g-----	-----a--a	-----	-c-----	-----t---
AgalGapCDNA	-ag-t-----	-----a---	--t-----	-----	---a--t---
SiniGapC	-ag-t-----	-----a---	-----	--g-t-----	---a-----
BovGapC	-gt--g-g-g	cc-tct-aag	gg--t-ct--	gctac-ct-a	ggaccag-t-
	851				900
DysGapC	ATCGTAGGCG	TGTCATA...	CGGTTCAATTG	TTTGACGCAA	CTCAAACATA
SpyGapC	-----cg	-a-----	-----	-----c-a-	-----
SeqGapC	-----cg	-a-----	-----	-----c-a-	-----
ParaUbGapC	-----t-ta	---t-t...	-----a	--c-----	-----
UberGapC	---a-c-ta	--g-t---	-----	-----	-----
AgalGapCDNA	-----t-ta	-t-----	-----	-----	-----
SiniGapC	-----ta	-t-t---	-----a	-----	-----
BovGapC	g--tcct-cg	ac-tca-cag	--a-a-tcac	-c-tc-a-ct	tcg-tg--gg

FIG. 6D



	901				950
DysGapC	AGTTATGGAA	GTTGACGGAT	CACAATTGGT	TAAAGTTGTA	TCATGGTATG
SpyGapC	---aatggaa	-----c---t	ca-----	-----a	-----
SeqGapC	---tatggaa	-----t---t	ca-----	-----a	-----
ParaUbGapC	---a-----	-----t---	-t-----a-	-----	-----
UberGapc	---a-----	-----t---	-t-----a-	-----	-----
AgalGapCDNA	---t-----	-----c-t-	-c-----	-----	-----c-
SiniGapC	---a-----	-----t---	-t-----	-----	-----
BovGapC	g-ctggc-t-	-ccctcaacg	-c--c--t--	c--gc-ca--	--c-----c-
	951				1000
DysGapC	ACAATGAAAT	GTCTTACACT	GCTCAACTTG	TTCGTACACT	TGAGTATTTT
SpyGapC	---c-----	-----	-----	-a-----t--	-----c
SeqGapC	---c-----	-----	-----	-----	-----
ParaUbGapC	---t-----	-----	-----	a-----	-----
UberGapc	---c-----	-----	---a-----	-----t--	-----
AgalGapCDNA	-t-c-----	---a-----	t-a-----	-----	-----
SiniGapC	---t-----	-----	-----	-----t--	-----
BovGapC	---t---t-	tggc---gc	aaa--gg---	-----	-----
	1001		1018		
DysGapC	GCAAAAAATCG	CTAAATAA			
SpyGapC	-----t-	-----			
SeqGapC	-----	-----			
ParaUbGapC	-----	-----			
UberGapc	-----	-----			
AgalGapCDNA	-----	-----			
SiniGapC	-----	-----			
BovGapC	-----	-----			

FIG. 6E





	1				50
DysGapC	MVVKVGINGF	GRIGRLAFRR	IQNVEGVEVT	RIND.LTDPN	MLAHLKLYDT
SpyGapC	-----	-----	---I-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
PUberGapC	-----	-----	-----	-----	-----
UberGapC	-----	-----	-----	-----	-----
AgalGapC	-----	-----	-----	-----	-----
IniaeGapC	-----	-----	-----	-----	-----
BovGapC	-----	-----vt-a	af-sgk-div	a---pfi-lh	ymvymfq--s
	51				100
DysGapC	TQGRFDGTVE	VKEGGFEVNG	NFIKVSAERD	PENIDWATDG	VEIVLEATGF
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----	-----
PUberGapC	-----	--d--d--	k-----k-	--q-----	-----
UberGapC	-----	--d-----	-----k-	-----	-----
AgalGapC	-----	-----	q-v-----e	-a-----	-----
IniaeGapC	-----	--d-----	s-v-----e	-a-----	-d-----
BovGapC	-h-k-n---k	aen-klvi-	ka-tifq--	-a--k-gda-	a-y-v-s--v
	101				150
DysGapC	FAKKEAAEKH	LHANGAKKVV	ITAPGGNDVK	TVVFNTNHDI	LDGTETVISG
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----p	-----	-----	qlfstltts-	-----
PUberGapC	---a-----	--e-----	-----d--	-----	-----
UberGapC	---a-----	-----	-----d--	-----	-----
AgalGapC	--s--k-gq-	i-e-----	-----	-----	-----
IniaeGapC	--s-a--q-	i-----	-----	---y-----	-----
BovGapC	-ttm-k-ga-	-.kg---r-i	-s--sa.-ap	mf-mgv--ek	ynn-lkiv-n

FIG. 7A



	151				200
DysGapC	ASCTTNCLAP	MAKALHDAFG	IQKGLMTTIH	AYTGDQMILD	GPHRGDDLRR
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----	-----	-----v-	-hrg-----
PUberGapC	-----	-----q-n--	v-----	-----	-----
UberGapC	-----	-----q-n--	v-----	-----	-----
AgalGapC	-----	-----q-n--	v-----	-----	-----
IniaeGapC	-----	-----q-n--	v-----	g-----v-	-----
BovGapC	-----	l--vih-h--	ive-----v-	-i-at-ktv-	--s-klw-d
	201				250
DysGapC	ARAGAAIVP	NSTGAAKAIG	LVIPELNGKL	DGAAQRVPVP	TGSVTELVVT
SpyGapC	-----	-----	-----	-----	-----
SeqGapC	-----	-----r--	-----	-----	-----
PUberGapC	-----n--	-----	-----	-----	-----av
UberGapC	-----s--	-----	-----	-----	-----av
AgalGapC	-----	-----	-----	-----	-----a-
IniaeGapC	-----a--	-----	-----	-----	-----av
BovGapC	g-ga-q--i-	a-----v-	k-----	t-m-f---t-	nv--vd-tcr
	251				300
DysGapC	LDKNVSVDEI	NAAMKAASND	S....FGYTE	DPIVSSDIVG	VSYGSLFDAT
SpyGapC	-----	-s-----	.....	-----	-----
SeqGapC	-----	-----	.....	-----	-----
PUberGapC	-n-et--e--	-sv---a--	....y---	-----	m-f-----
UberGapC	-e-et--e--	-----a--	....y---	-----i-	ma-----
AgalGapC	-e-d-t-e-v	-----a--	....y---	-----	i-----
IniaeGapC	-e-dt--e--	-----a--	....y---	-a-----	i-----
BovGapC	-e-paky---	kkvv-q--eg	plkgilg---	-qv--c-fns	dths-t---g
	301				341
DysGapC	QTKVMEVDGS	QLVKVVSWDY	NEMSYTAQLV	RTLEYFAKIA	K
SpyGapC	-----	-----	-----	-----	-
SeqGapC	-----	-----	-----	-----	-
PUberGapC	----qt---n	-----	-----d	-----	-
UberGapC	----qt---n	-----	-----	-----	-
AgalGapC	----qt---n	-----	-----s--	-----	-
IniaeGapC	----qt---n	-----	-----	-----	-
BovGapC	agial...nd	hf--li---	--fg-sk---	-----	-

FIG. 7B

# Peptide Structure Results

Peptide Structure of: DysGapC

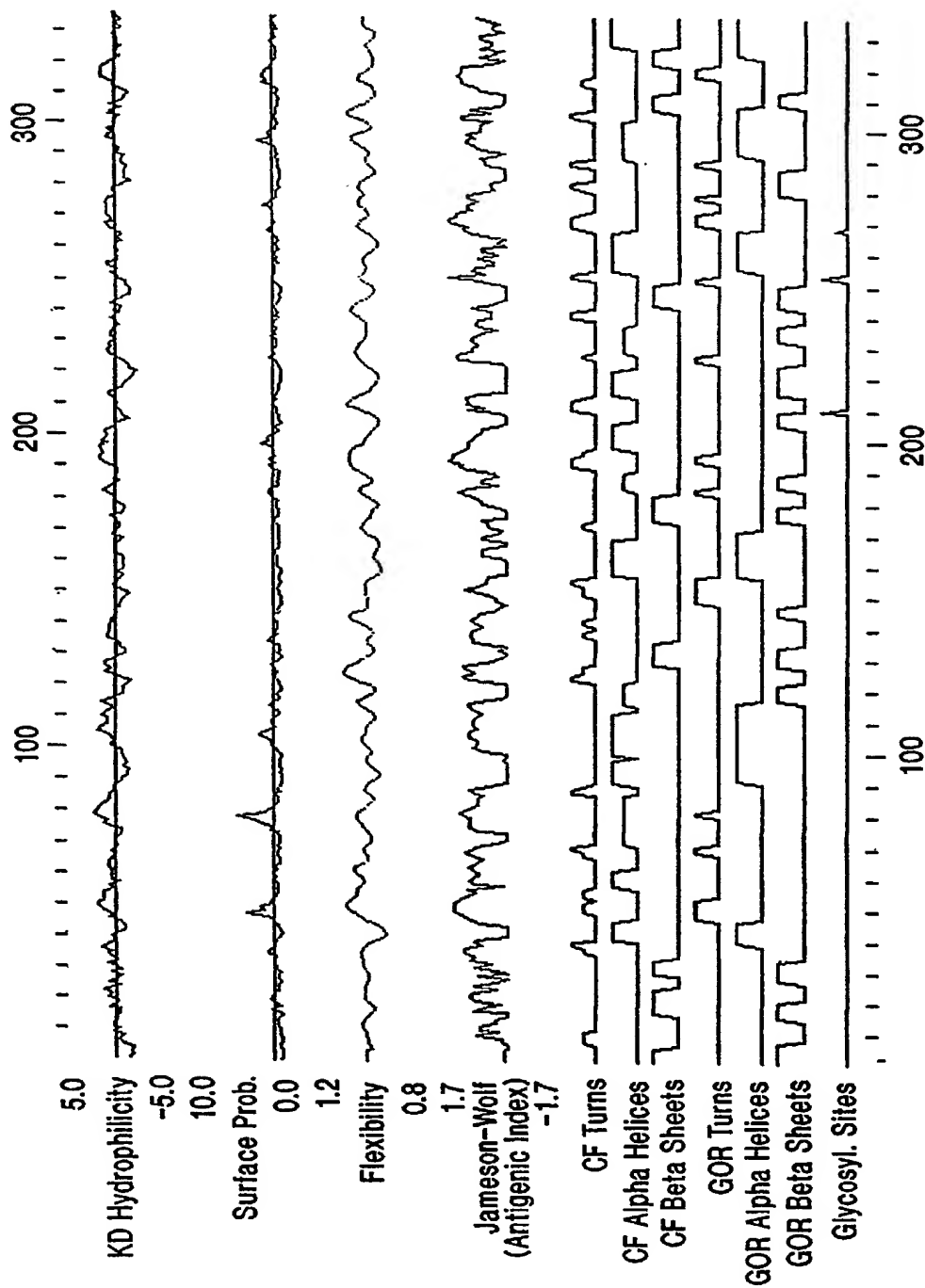


FIG. 8



09878781.09.1002

# Peptide Structure Results

Peptide Structure of: AgalGapC

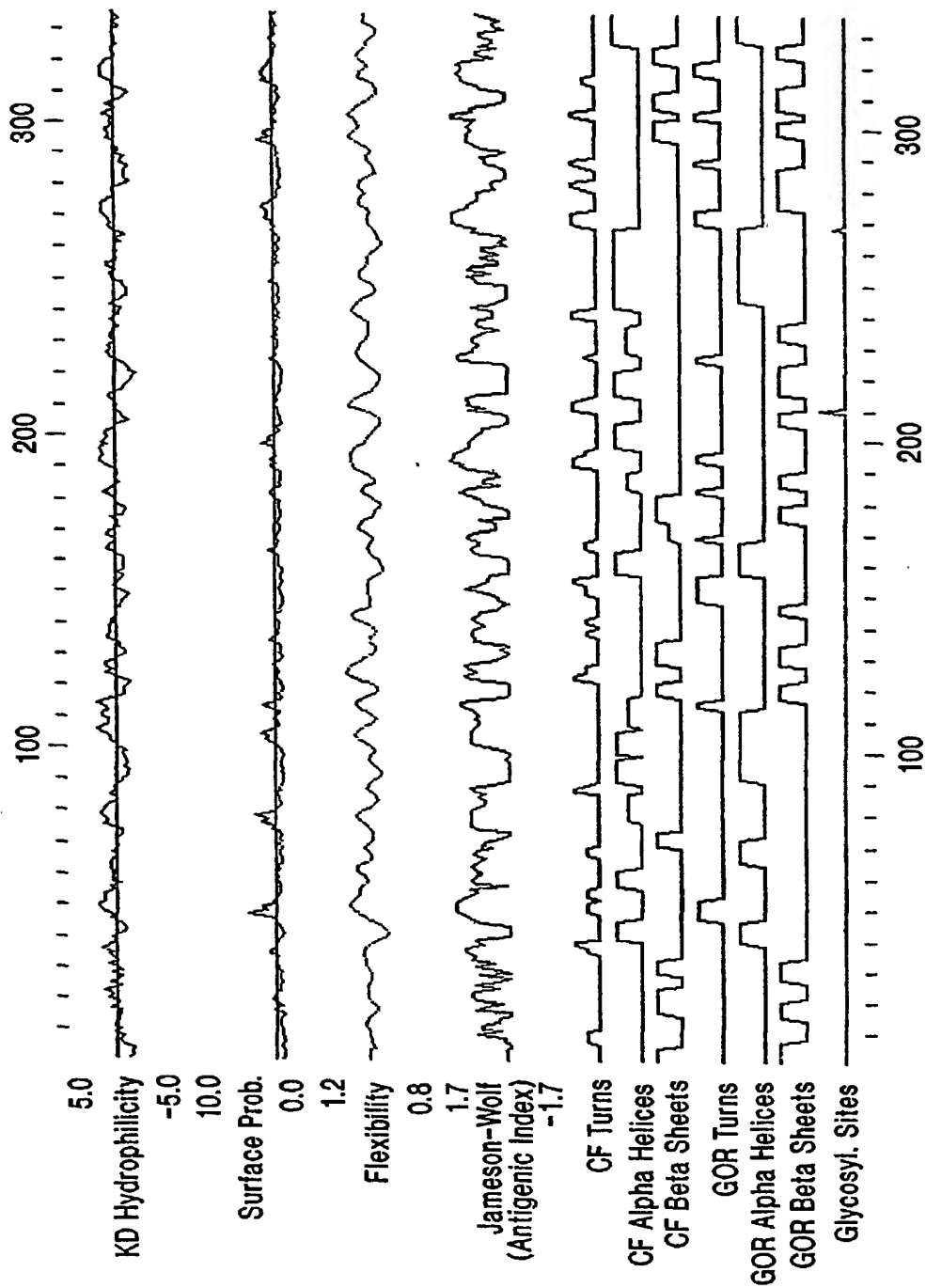


FIG. 9



09876543 2001002

# Peptide Structure Results

Peptide Structure of: UberGapC

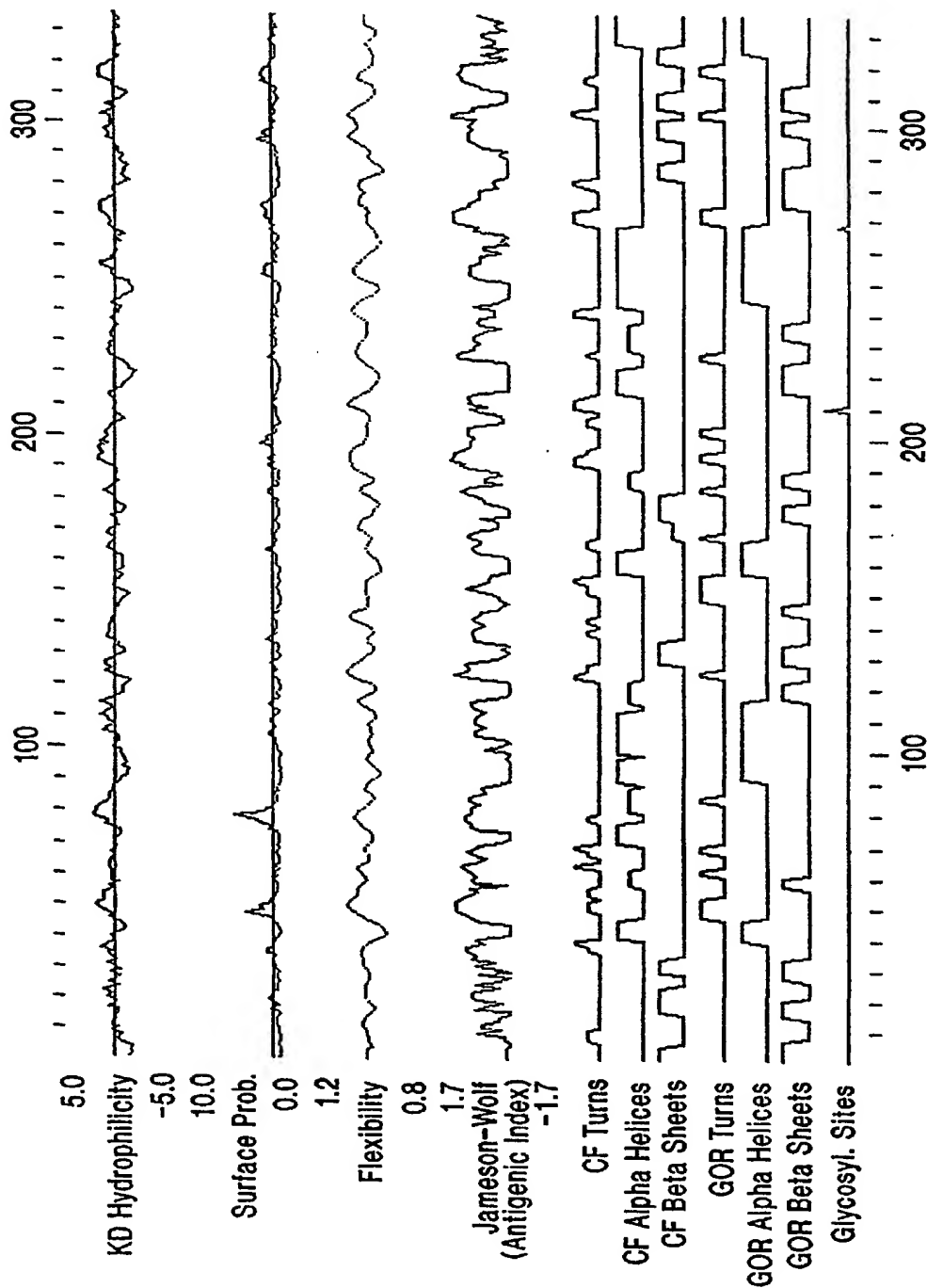


FIG. 10



09678781.091012

# Peptide Structure Results

Peptide Structure of: PÜberGapC

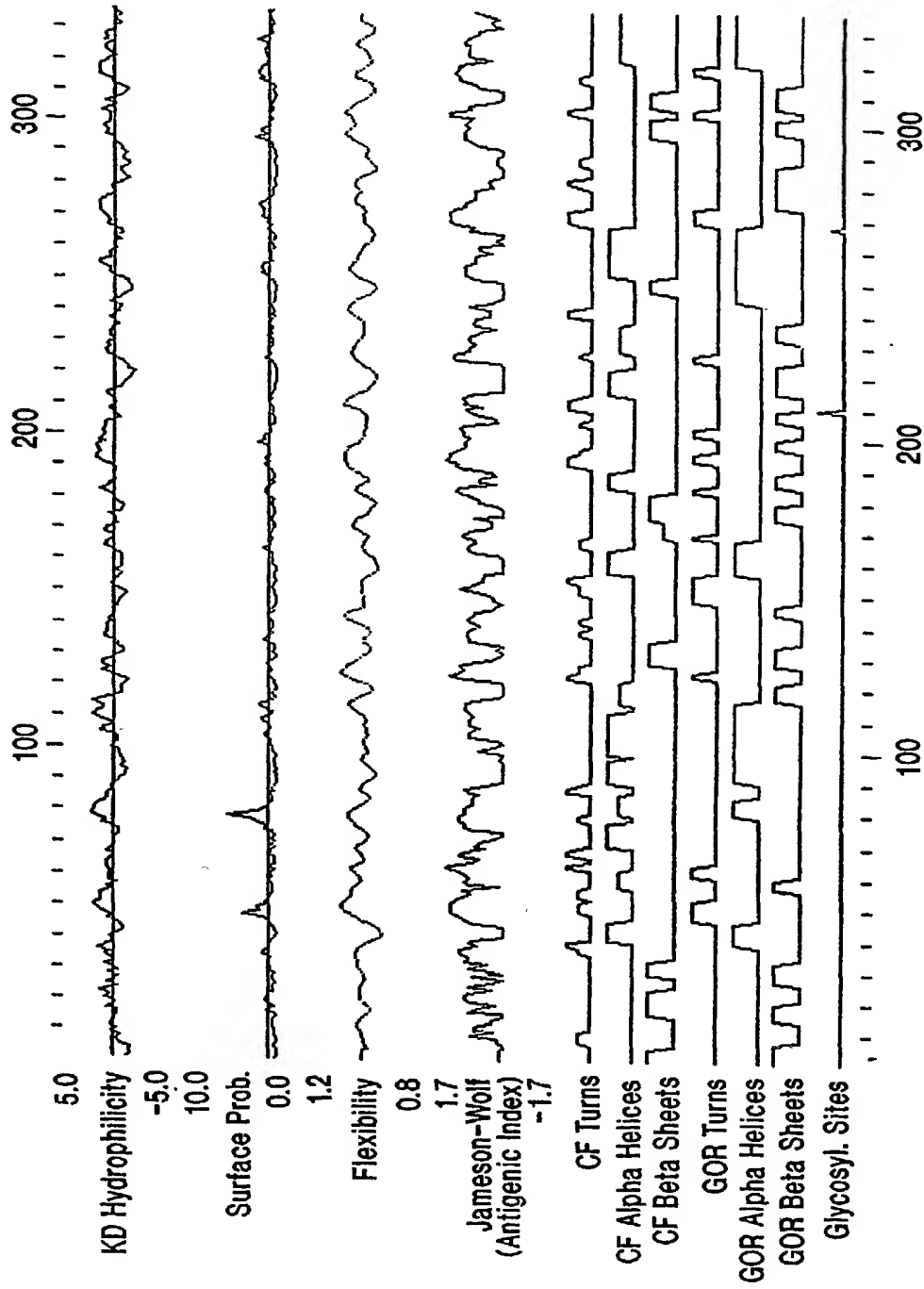


FIG. 11



09078791, 091002

# Peptide Structure Results

Peptide Structure of: IniaeGapC

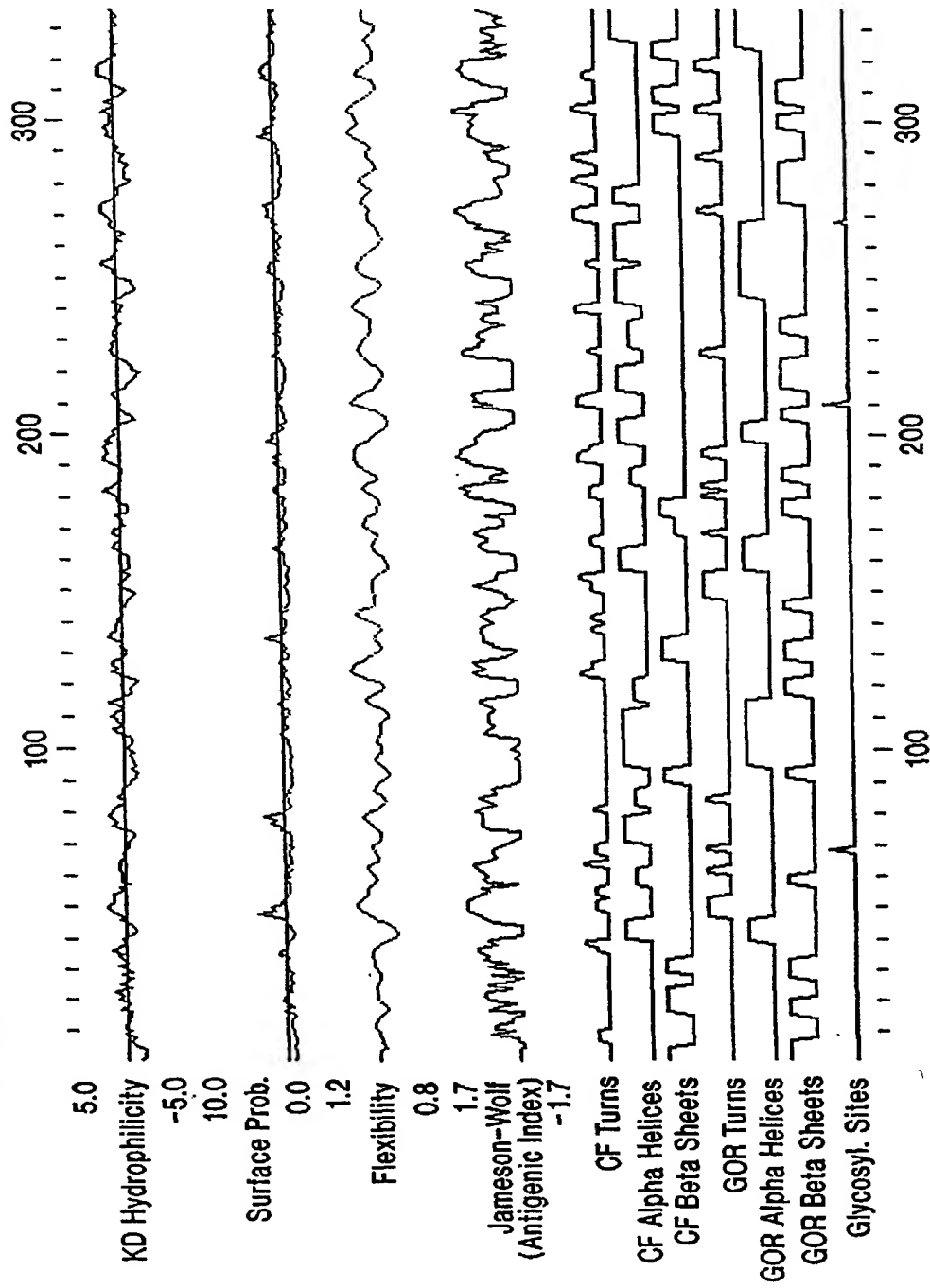


FIG. 12



09978781, 09978782

# Peptide Structure Results

Peptide Structure of: DysGapC

○ KD Hydrophilicity  $\geq 1.3$   
 ◇ KD Hydrophobicity  $\geq 1.3$

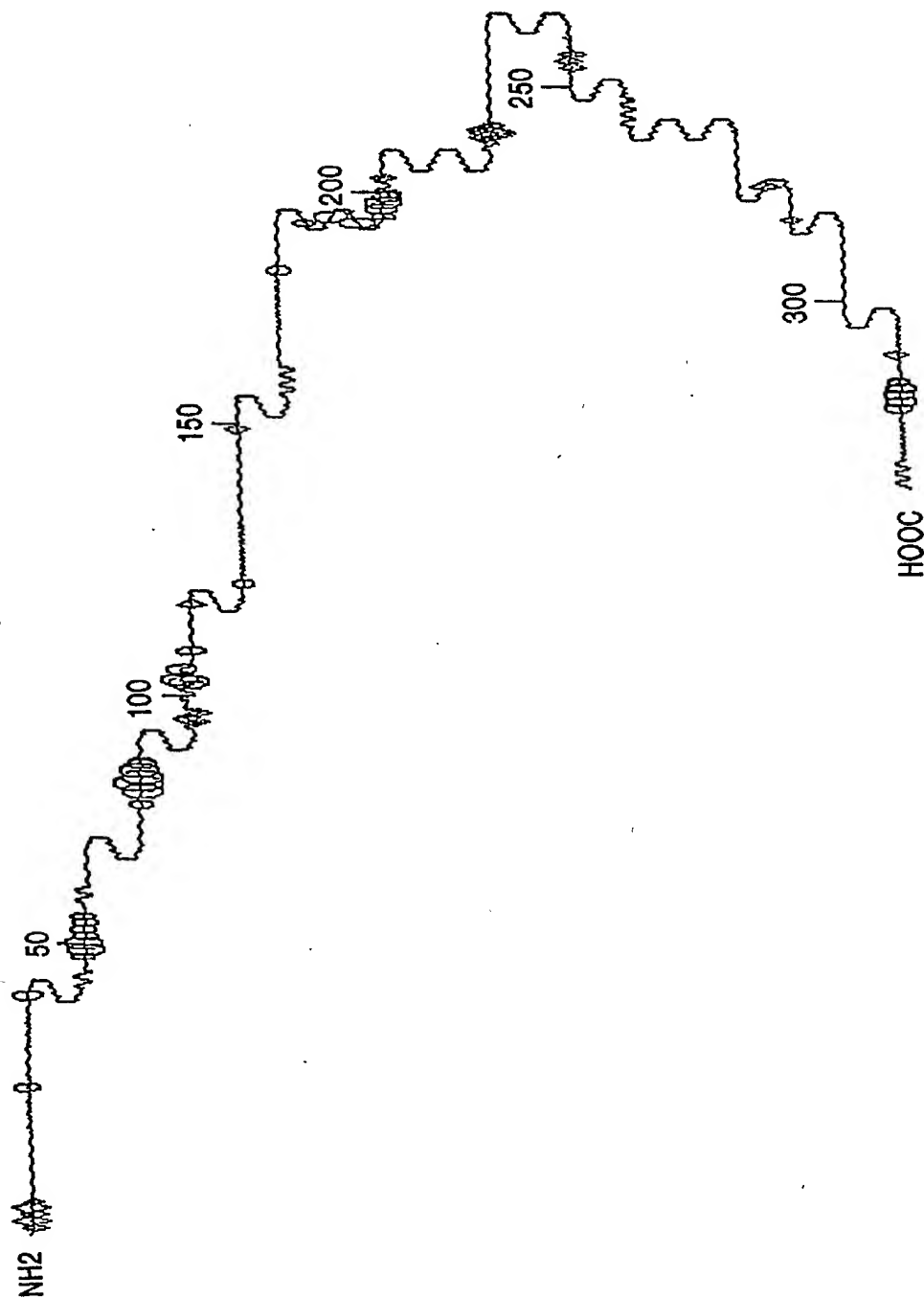
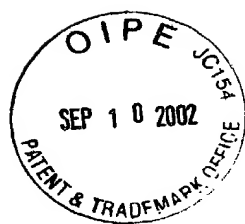


FIG. 13



09078781 . 09.1002



# Peptide Structure Results

Peptide Structure of: AgalGapC

○ KD Hydrophilicity  $\geq 1.3$   
 ◇ KD Hydrophobicity  $\geq 1.3$

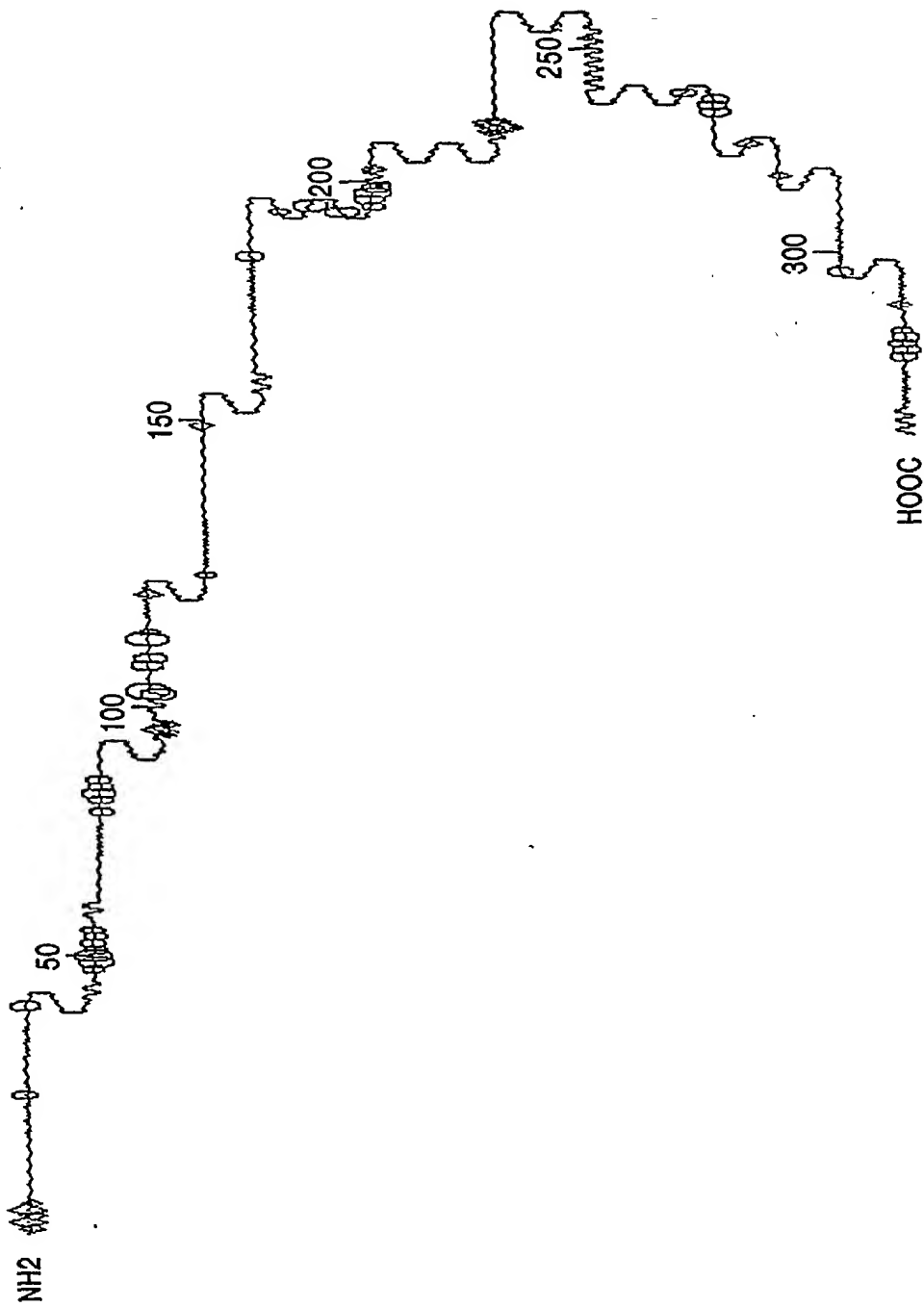


FIG. 14



09829794.091002

# Peptide Structure Results

Peptide Structure of: UberGapC

○ KD Hydrophilicity  $\geq 1.3$   
 ◇ KD Hydrophobicity  $\geq 1.3$

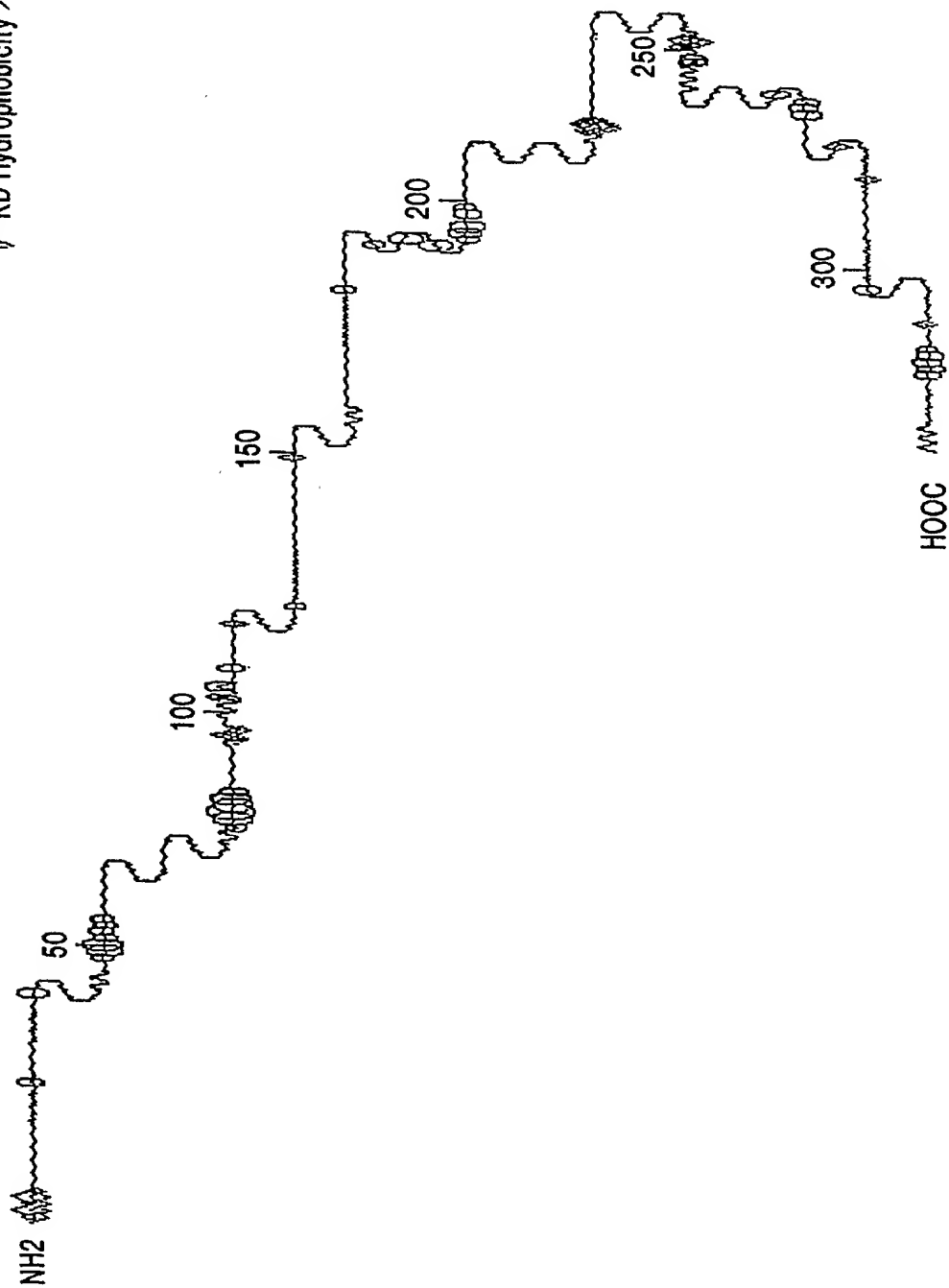


FIG. 15



09070751.091002

# Peptide Structure Results

Peptide Structure of: PUberGapC

○ KD Hydrophilicity  $\geq 1.3$   
 ◇ KD Hydrophobicity  $\geq 1.3$

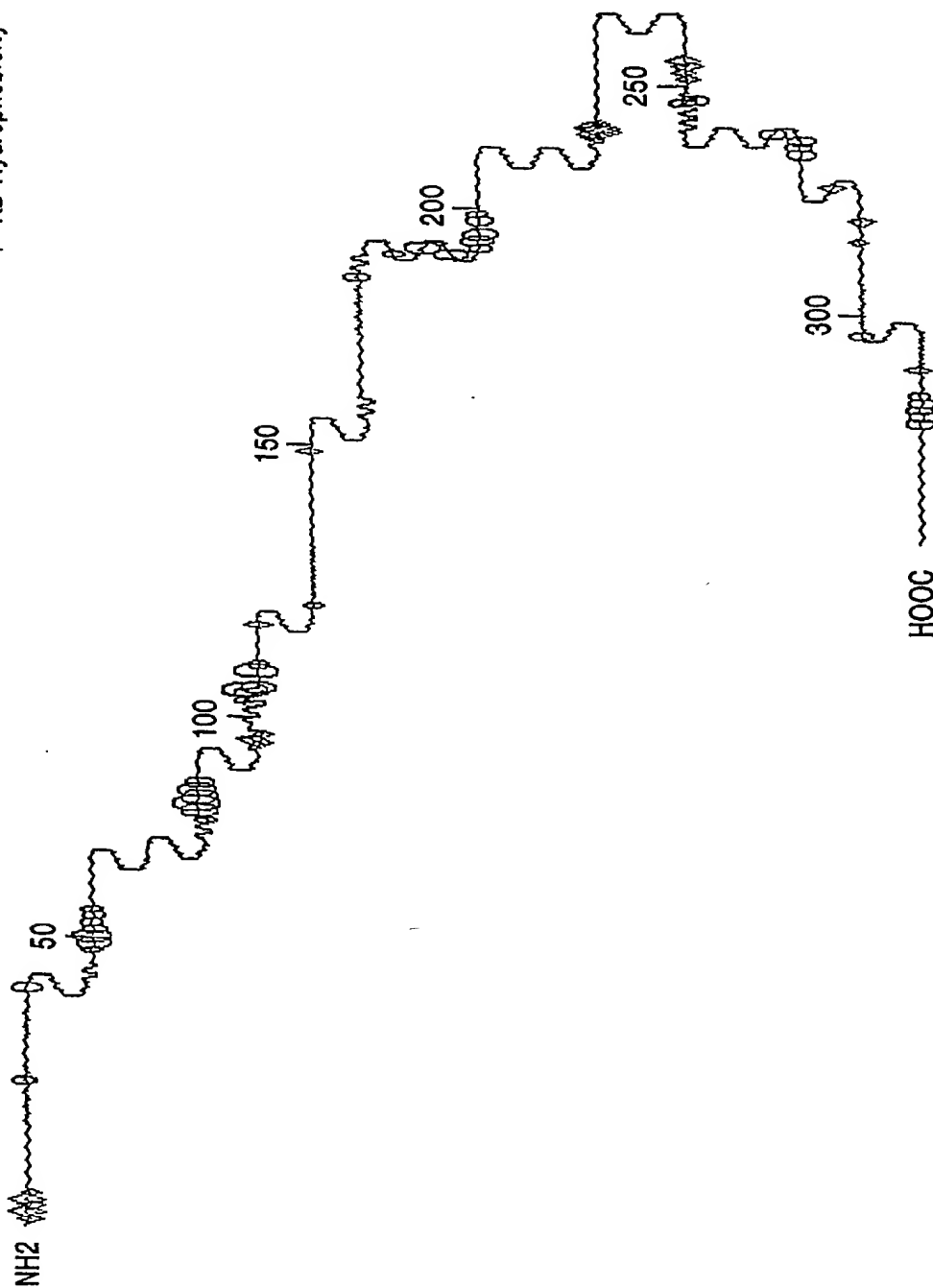


FIG. 16



09678781.091012



Peptide Structure Results

Peptide Structure of: IniaeGapC

○ KD Hydrophilicity  $\geq 1.3$   
◇ KD Hydrophobicity  $\geq 1.3$

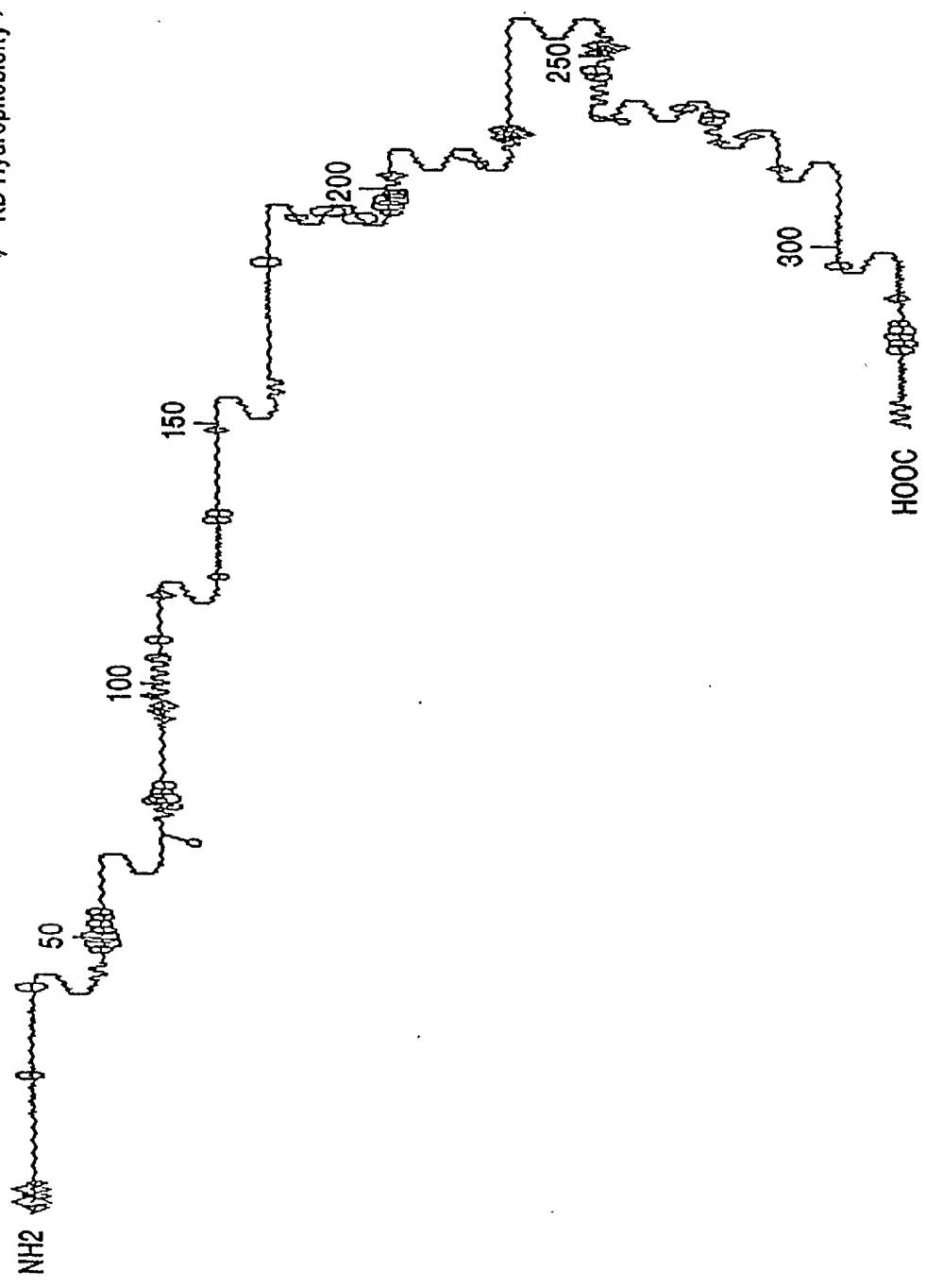


FIG. 17



09324791.091002

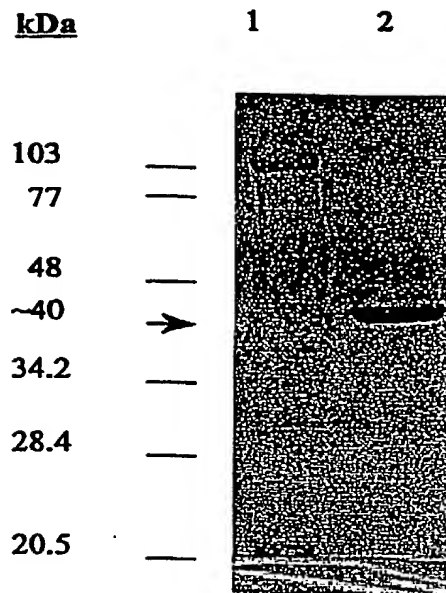


FIG. 18

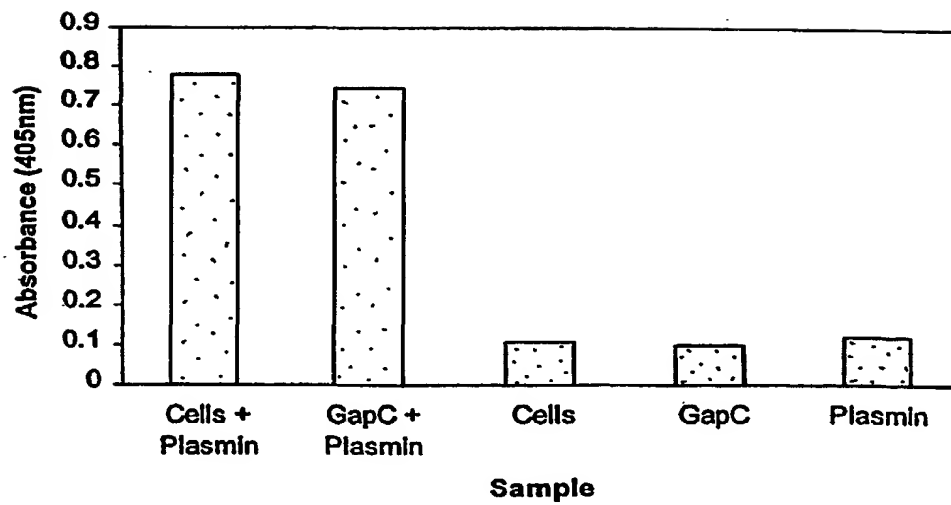


FIG. 19



110078781.09.1002

Percentage of quaters infected with *S. dysgalactiae* per group

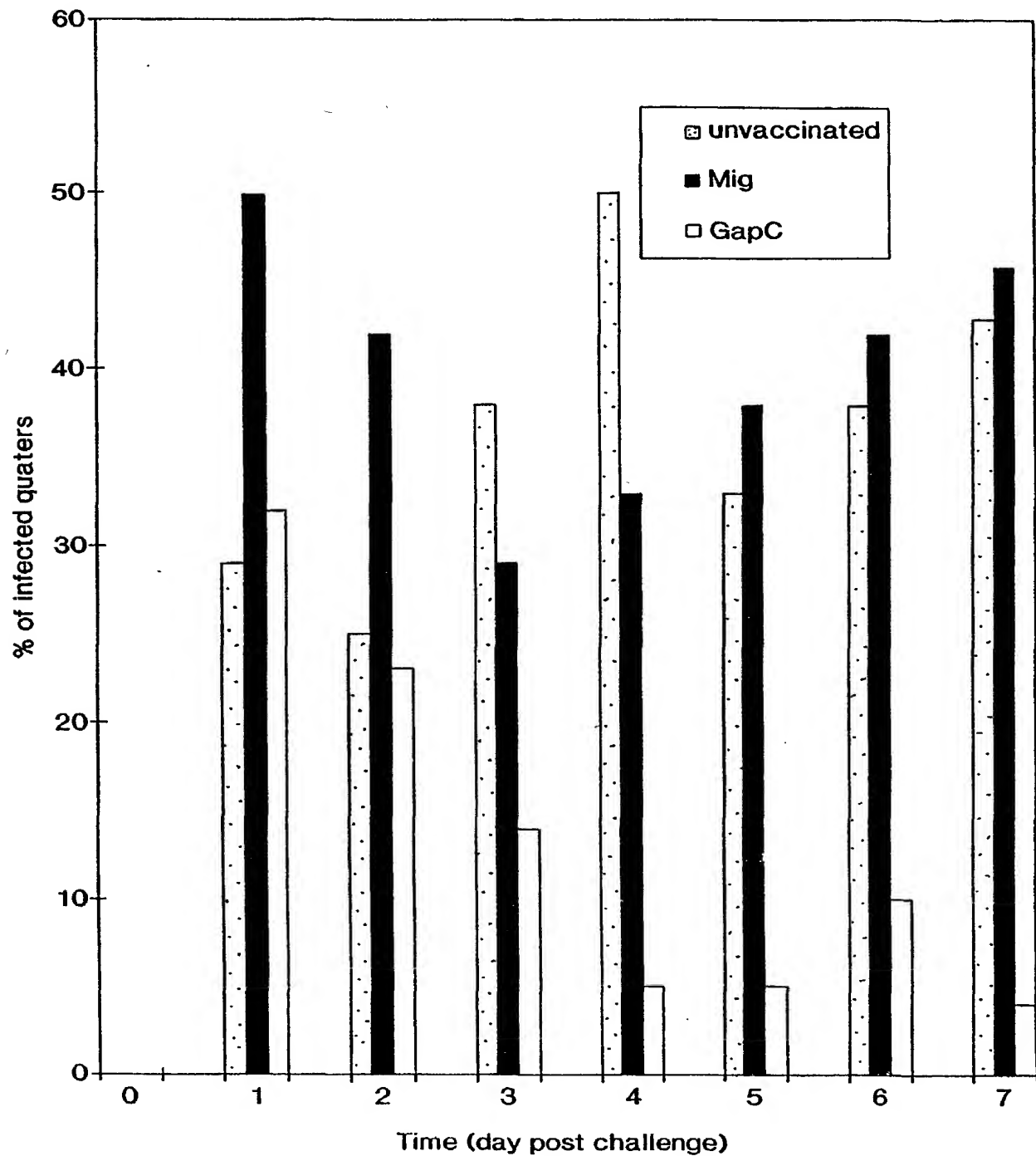


FIG. 20



09278791.001002

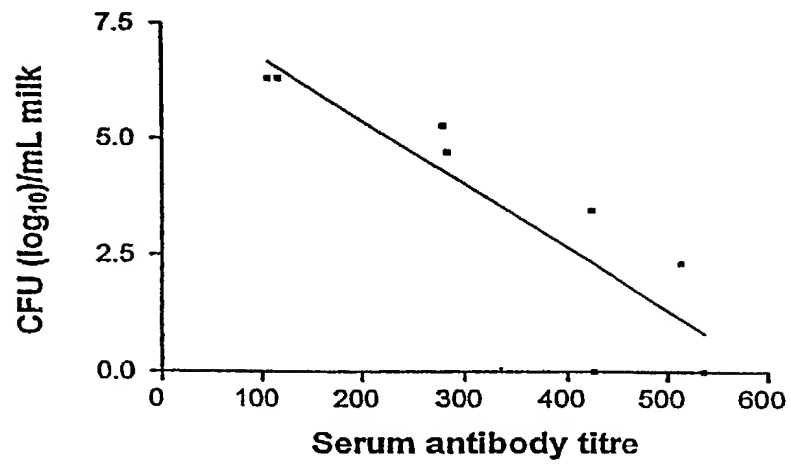


FIG. 21

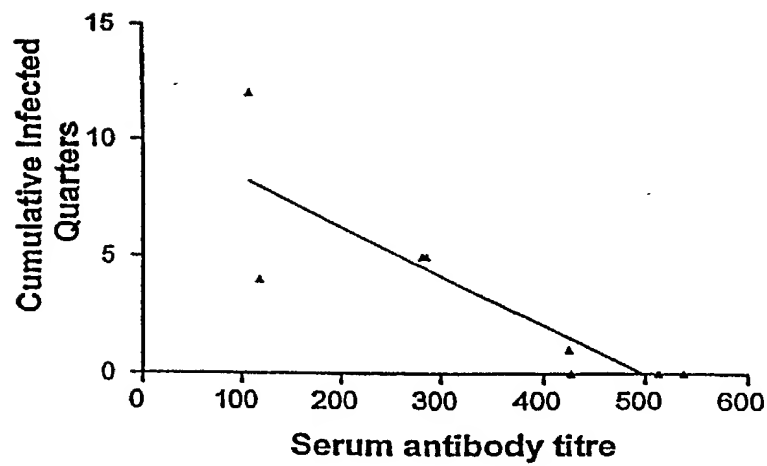


FIG. 22

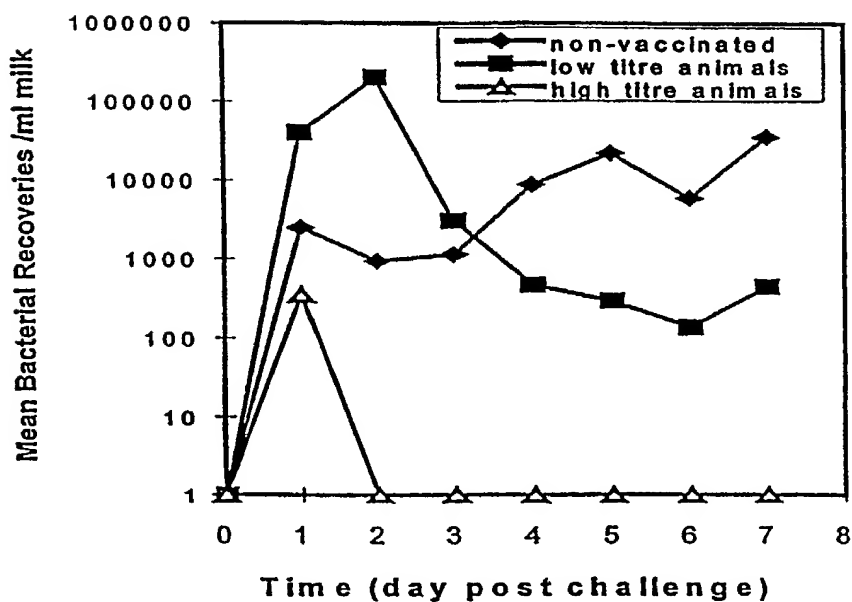


FIG. 23

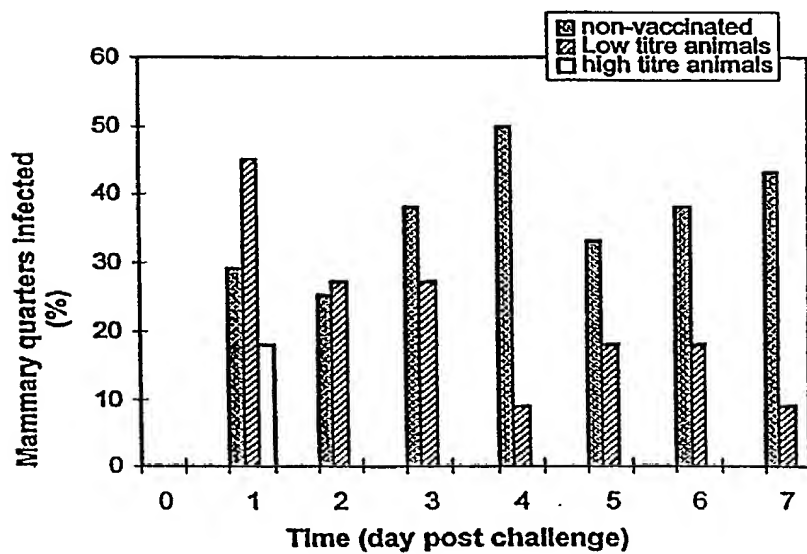


FIG. 24





Mean Somatic Cell Counts (SCC) per group

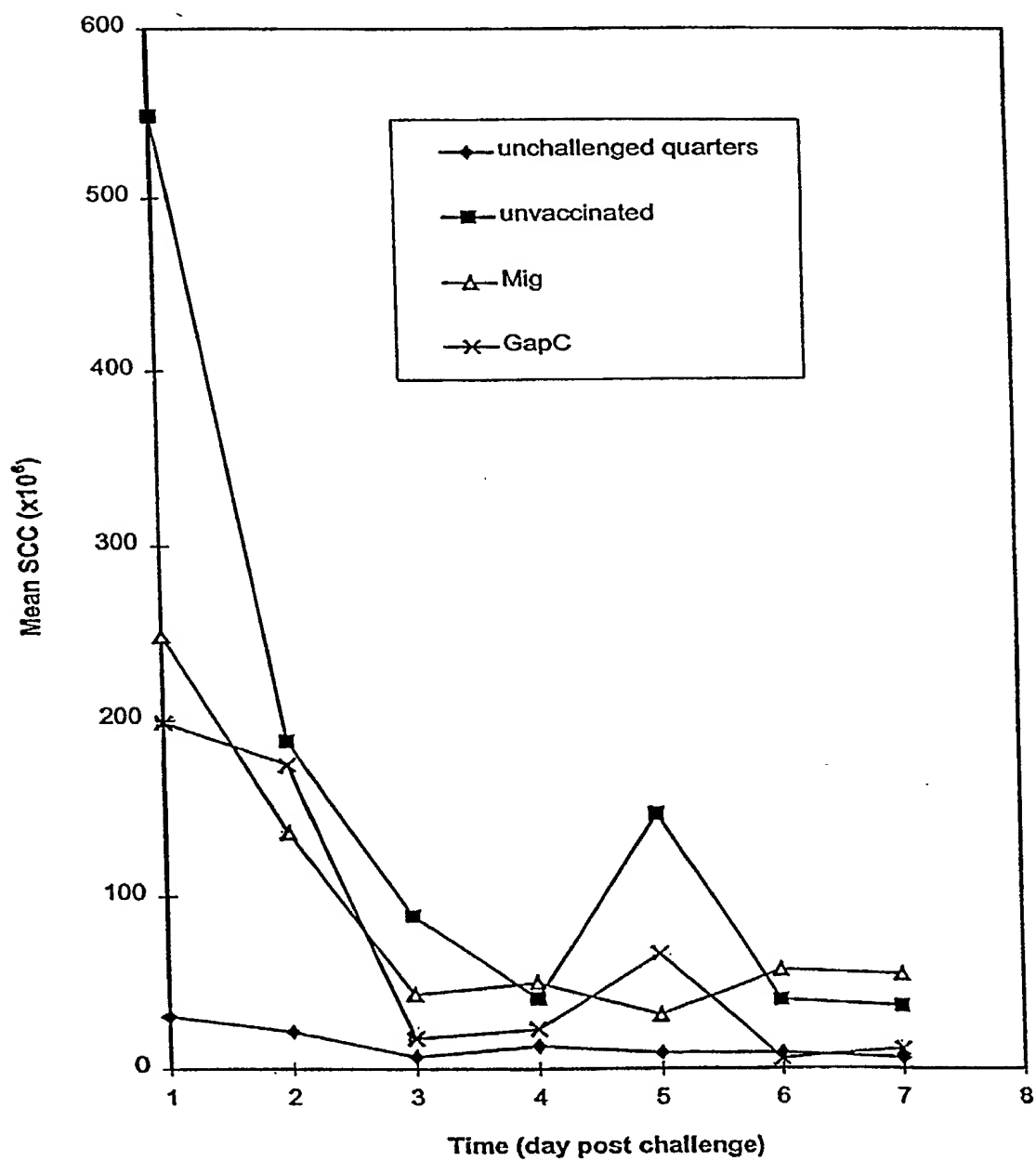
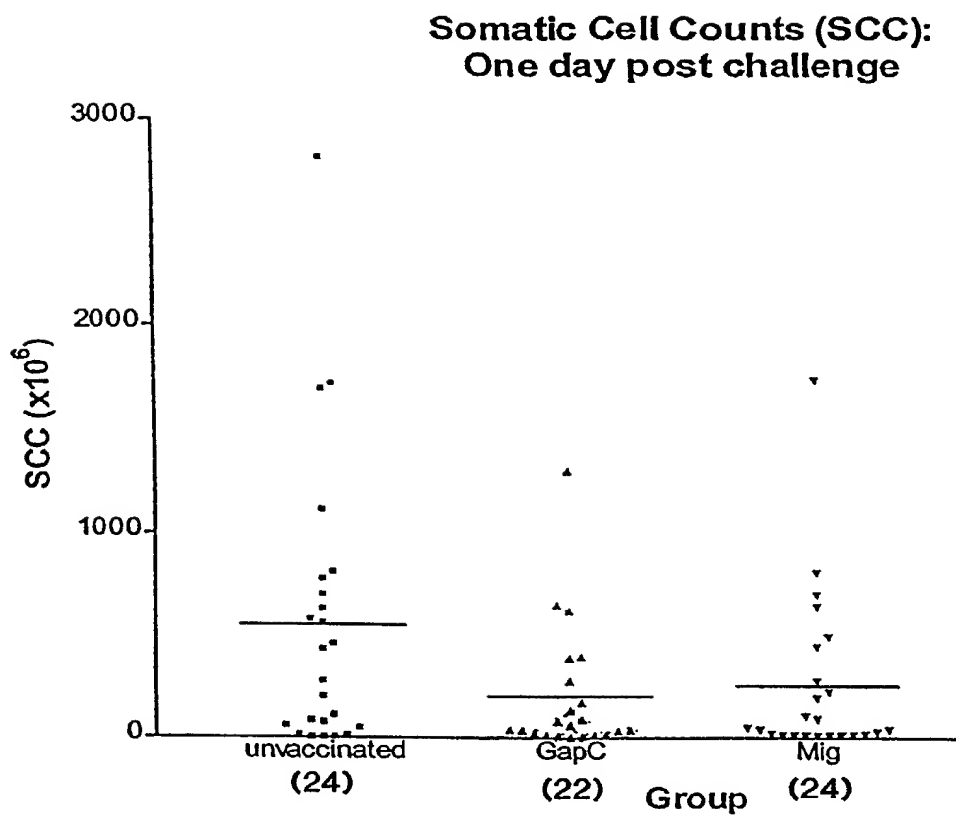


FIG. 25



**FIG. 26**

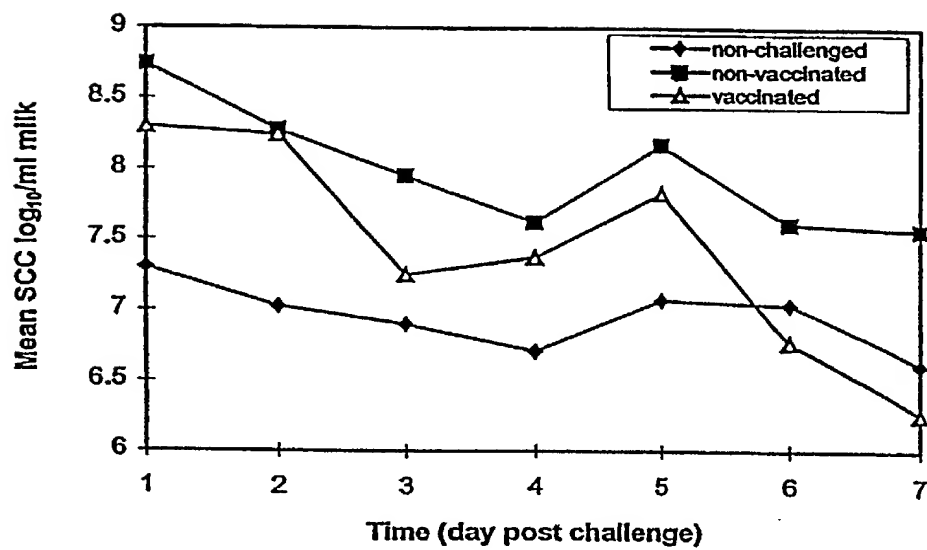


FIG. 27